

PLAYING EPIDEMIOLOGICAL TELEPHONE: IN-HOST EVOLUTION OF INFLUENZA A VIRUS

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ABSTRACT. Like other RNA viruses, Influenza A virus (IAV) has a high mutation rate and large in-host population size, and is thus capable of rapid evolutionary change. While large-scale antigenic changes have been well-studied at the epidemiological scale, we tackle the underlying small-scale question: how does IAV, as received at the start of an infection in a single individual, differ from IAV as transmitted from that individual to others? To address this, we couple a system of ordinary differential equations, describing the in-host dynamics of IAV, to a branching process describing the fate of de novo mutant lineages within the host. This semi-stochastic approach is necessary because IAV can reach extremely high copy numbers in a single infected host, while the transmission bottleneck may involve as few as ten viral particles. We predict that as many as 20-30% of the viral particles transmitted to each recipient may carry mutations generated de novo in the donor individual.

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